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AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

Claims 1–9 (Canceled).

- 10. (Withdrawn Currently amended): A computerimplemented method of identifying a drug candidate compound for the treatment of an angiogenesis mediated disorder, comprising:
 - (a) providing X, Y and Z atomic structure coordinates set forth in any of Figures 7-304 for all or a portion of a crystalline form of an HPTPbeta catalytic domain [SEQ ID NO: 7];
 - (b) determining a three-dimensional structure of all or a portion of a crystalline form of an HPTPbeta catalytic domain [SEQ ID NO: 7] from said X, Y and Z coordinates;
 - (c) imaging said three-dimensional structure of all or a portion of a crystalline form of an HPTPbeta catalytic domain [SEQ ID NO: 7];
 - (d) positioning one or more candidate compounds at one or more areas of said imaged three-dimensional structure by using binding mode(s) of said one or more candidate compounds with said area(s) of said imaged three-dimensional structure; and
 - (e) identifying from said one or more candidate compounds those that bind or modulate HPTPbeta as drug candidate compounds useful for the treatment of an angiogenesis mediated disorder.
- 11. (Withdrawn): The method of claim 10, further comprising determining the one or more locations or binding geometries

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of said positioned one or more candidate compounds relative to any of said X, Y and Z atomic structure coordinates.

- 12. (Withdrawn): The method of claim 10, further comprising assembling fragments of said one or more candidate compounds together to create an assembled compound.
- 13. (Withdrawn): The method of claim 12, further comprising analyzing the ability of said assembled compound to bind or modulate HPTPbeta in an *in vivo* or *in vitro* assay.
- 14. (Withdrawn): The method of claim 10, wherein said one or more candidate compounds or portion(s) thereof are HPTPbeta agonists.
- 15. (Withdrawn): The method of claim 14, further comprising analyzing the ability of said one or more candidate compounds to bind or modulate HPTPbeta in an *in vivo* or *in vitro* assay.
- 16. (Withdrawn): The method of claim 10, wherein said one or more candidate compounds or portion(s) therof are HPTPbeta antagonists.
- 17. (Withdrawn): The method of claim 16, further comprising analyzing the ability of said one or more candidate compounds to bind or modulate HPTPbeta in an *in vivo* or *in vitro* assay.
- 18. (Withdrawn): The method of claim 10, wherein said X, Y and Z atomic structure coordinates of said three-dimensional structure are HPTPbeta binding sites or combinations thereof.
- 19. (Withdrawn): The method of claim 10, wherein said one or more candidate compounds are positioned at at least one of the P(0), P(+1) and P(-1) binding sites of HPTPbeta.

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- 21. (Withdrawn): The method of claim 18, wherein said one or more candidate compounds are positioned at at least amino acid residues 76-80, 48-66, 284-292 and 212-214 of SEQ ID NO: 7.
- 22. (Withdrawn): The method of claim 18, wherein said one or more candidate compounds are positioned at at least amino acid residues 69-76, 119-123 and 149-154 of SEQ ID NO: 7.
- 23. (Withdrawn): The method of claim 10, wherein said crystalline form of an HPTPbeta catalytic domain [SEQ ID NO: 7] has unit cell dimensions of approximately a=39 Å, b=71Å, c=120 Å, α =90°, β =90°, γ =90° in the space group P2₁2₁2₁.
- 24. (Withdrawn): The method of claim 10, wherein said crystalline form of an HPTPbeta catalytic domain [SEQ ID NO: 7] has unit cell dimensions of approximately a=62 Å, b=72Å, c=70 Å, α =90°, β =93°, γ =90° in the space group P2₁.
- 25. (Currently amended): A method of identifying a drug candidate compound for the treatment of an angiogenesis mediated disorder, comprising:
 - (a) imaging, through the use of computer modeling of X, Y and Z atomic structure coordinates set forth in Figures 202-252, a crystalline form of an HPTPbeta catalytic domain [SEQ ID NO: 7] using unit cell dimensions of approximately a=39 Å, b=71Å, c=120 Å, α =90°, β =90°, γ =90° in the space group P2₁2₁2₁;

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(b) computationally positioning a drug candidate compound at one or more areas of said imaged HPTPbeta catalytic domain [SEQ ID NO: 7] by using a binding mode of said drug candidate compound with said area(s) of said imaged HPTPbeta catalytic domain; and

- (c) analyzing the ability of said drug candidate compound to bind or modulate HPTPbeta in an *in vivo* or *in vitro* assay.
- 26. (Currently amended): A method of identifying a drug candidate compound for the treatment of an angiogenesis mediated disorder, comprising:
 - (a) imaging, through the use of computer modeling of X, Y and Z atomic structure coordinates set forth in Figures 7-102, a crystalline form of an HPTPbeta catalytic domain [SEQ ID NO: 7] using unit cell dimensions of approximately a=62 Å, b=72 Å, c=70 Å, α =90°, β =93°, γ =90° in the space group P2₁;
 - (b) computationally positioning a drug candidate compound at one or more areas of said imaged HPTPbeta catalytic domain [SEQ ID NO: 7] by using a binding mode of said drug candidate compound with said area(s) of said imaged HPTPbeta catalytic domain; and
 - (c) analyzing the ability of said drug candidate compound to bind or modulate HPTPbeta in an *in vivo* or *in vitro* assay.
- 27. (Previously presented): The method according to claim 25, wherein said drug candidate compound is positioned at at least amino

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acid residues 152, 74-77, 209-214, 244-253, 288-290 and 293 of SEQ ID NO: 7.

- 28. (Previously presented): The method according to claim 26, wherein said drug candidate compound is positioned at at least amino acid residues 152, 74-77, 209-214, 244-253, 288-290 and 293 of SEQ ID NO: 7.
- 29. (Previously presented): The method according to claim 25, wherein said drug candidate compound is positioned at at least amino acid residues 76-80, 48-66, 284-292 and 212-214 of SEQ ID NO: 7.
- 30. (Previously presented): The method according to claim 26, wherein said drug candidate compound is positioned at at least amino acid residues 76-80, 48-66, 284-292 and 212-214 of SEQ ID NO: 7.
- 31. (Previously presented): The method according to claim 25, wherein said drug candidate compound is positioned at at least amino acid residues 69-76, 119-123 and 149-154 of SEQ ID NO: 7.
- 32. (Previously presented): The method according to claim 26, wherein said drug candidate compound is positioned at at least amino acid residues 69-76, 119-123 and 149-154 of SEQ ID NO: 7.